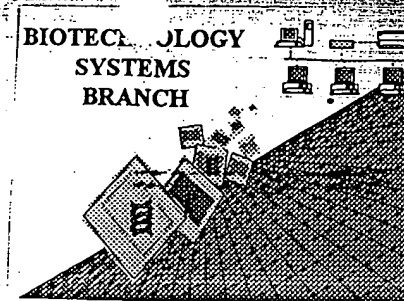


C Winkler

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/254,966

Source: 1648

Date Processed by STIC: 01-25-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/254,966

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/254,966

DATE: 01/25/2001
TIME: 23:33:06

INPUT SET: S35457.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information:

move response to same line.

(i) APPLICANT:

~~(A) NAME: Bayer Aktiengesellschaft~~

Delete

(ii) TITLE OF INVENTION: Immunogenic Peptides of Foot-and-Mouth Disease Viruses

(iii) NUMBER OF SEQUENCES: 48

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Bayer Corporation

(B) STREET: 100 Bayer Road

(C) CITY: Pittsburgh

(D) STATE: Pennsylvania

(E) ZIP CODE: 15205-9741

(F) COUNTRY: U.S.A.

Does Not Comply
Corrected Diskette Needed

pp. 1-21

(v) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS/Windows 95

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

~~(A) CURRENT APPLICATION NUMBER: 09/254,966~~

~~(B) CURRENT APPLICATION FILING DATE: March 16, 1999~~

~~(C) PRIOR APPLICATION NUMBER: PCT/EP97/04866~~

~~(D) PRIOR APPLICATION FILING DATE: September 8, 1997~~

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP97/04866

(B) FILING DATE: 8-SEPT-1997

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:06

INPUT SET: S35457.raw

molecule Type: peptide

--> 40 (ii) ~~TYPE OF MOLECULE: peptide~~
41
42 (iii) HYPOTHETICAL: NO
43
44 (iv) ANTI-SENSE: YES
45
46 (v) FRAGMENT TYPE: internal fragment
47
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
49
50 Glu Arg Val His Val Met Arg Lys Thr Lys Leu Ala Pro Thr Val
51 1 8 5 10 10 15 15
52

*This error is global.
Please check and correct
each of the 48 sequences.*

53 (2) INFORMATION FOR SEQ ID NO: 2:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 15 amino acids
57 (B) TYPE: amino acid
58 (C) STRANDEDNESS: single-stranded
59 (D) TOPOLOGY: linear
60 *molecule Type: Peptide*
--> 61 (ii) ~~TYPE OF MOLECULE: peptide~~
62
63 (iii) HYPOTHETICAL: NO
64
65 (iv) ANTI-SENSE: YES
66
67 (v) FRAGMENT TYPE: internal fragment
68
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
70
71 Met Arg Lys Thr Lys Leu Ala Pro Thr Val Ala His Gly Val Phe
72 1 5 5 10 10 15 15
73

*Misaligned amino
acid numbering. Use "spaces"
instead of "tabs". See
#4 on Error Summary
Sheet. This error
is also
global. Please
check and
correct each
sequence.*

74 (2) INFORMATION FOR SEQ ID NO: 3:
75
76 (i) SEQUENCE CHARACTERISTICS:
77 (A) LENGTH: 15 amino acids
78 (B) TYPE: amino acid
79 (C) STRANDEDNESS: single-stranded
80 (D) TOPOLOGY: linear
81 *molecule Type: peptide*
--> 82 (ii) ~~TYPE OF MOLECULE: peptide~~
83
84 (iii) HYPOTHETICAL: NO
85
86 (iv) ANTI-SENSE: YES
87
88 (v) FRAGMENT TYPE: internal fragment
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:07

INPUT SET: S35457.raw

91
92 Leu Ala Pro Thr Val Ala His Gly Val Phe Asn Pro Glu Phe Gly
93 1 5 10 15
94

Error #4 refer to p.2

95 (2) INFORMATION FOR SEQ ID NO: 4:

96

97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 15 amino acids

99 (B) TYPE: amino acid

100 (C) STRANDEDNESS: single-stranded

101 (D) TOPOLOGY: linear

102

--> 103 (ii) ~~TYPE OF MOLECULE: peptide~~

104

105 (iii) HYPOTHETICAL: NO

106

107 (iv) ANTI-SENSE: YES

108

109 (v) FRAGMENT TYPE: internal fragment

110

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

112

113 Arg Cys Ala Ala Asp Tyr Ala Ser Arg Leu His Ser Val Leu Gly

114 1 5 10 15

115

Error #4

116 (2) INFORMATION FOR SEQ ID NO: 5:

117

118 (i) SEQUENCE CHARACTERISTICS:

119 (A) LENGTH: 15 amino acids

120 (B) TYPE: amino acid

121 (C) STRANDEDNESS: single-stranded

122 (D) TOPOLOGY: linear

123

--> 124 (ii) ~~TYPE OF MOLECULE: peptide~~

125

126 (iii) HYPOTHETICAL: NO

127

128 (iv) ANTI-SENSE: YES

129

130 (v) FRAGMENT TYPE: internal fragment

131

132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

133

134 Asn Gly Thr Val Gly Pro Glu Val Glu Ala Ala Leu Lys Leu Met

135 1 5 10 15

136

Error #4

137 (2) INFORMATION FOR SEQ ID NO: 6:

138

139 (i) SEQUENCE CHARACTERISTICS:

140 (A) LENGTH: 15 amino acids

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:07

INPUT SET: S35457.raw

141 (B) TYPE: amino acid
142 (C) STRANDEDNESS: single-stranded
143 (D) TOPOLOGY: linear
144
--> 145 ~~(ii) TYPE OF MOLECULE: peptide~~
146
147 (iii) HYPOTHETICAL: NO
148
149 (iv) ANTI-SENSE: YES
150
151 (v) FRAGMENT TYPE: internal fragment
152
153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
154
155 Glu Lys Arg Glu Tyr Lys Phe Val Cys Gln Thr Phe Leu Lys Asp
156 1 5 10 15
157

Error #4

158 (2) INFORMATION FOR SEQ ID NO: 7:
159
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 15 amino acids
162 (B) TYPE: amino acid
163 (C) STRANDEDNESS: single-stranded
164 (D) TOPOLOGY: linear
165
--> 166 ~~(ii) TYPE OF MOLECULE: peptide~~
167
168 (iii) HYPOTHETICAL: NO
169
170 (iv) ANTI-SENSE: YES
171
172 (v) FRAGMENT TYPE: internal fragment
173
174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
175
176 Ala Gln Met His Ser Asn Asn Gly Pro Gln Ile Gly Ser Ala Val
177 1 5 10 15
178

Error #4

179 (2) INFORMATION FOR SEQ ID NO: 8:
180
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 15 amino acids
183 (B) TYPE: amino acid
184 (C) STRANDEDNESS: single-stranded
185 (D) TOPOLOGY: linear
186
--> 187 ~~(ii) TYPE OF MOLECULE: peptide~~
188
189 (iii) HYPOTHETICAL: NO
190
191 (iv) ANTI-SENSE: YES

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:07

INPUT SET: S35457.raw

192
193 (v) FRAGMENT TYPE: internal fragment
194
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
196
197 Ile Gly Ser Ala Val Gly Cys Asn Pro Asp Val Asp Trp Gln Arg
198 1 5 10 15
199

Error #4

200 (2) INFORMATION FOR SEQ ID NO: 9:
201
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 15 amino acids
204 (B) TYPE: amino acid
205 (C) STRANDEDNESS: single-stranded
206 (D) TOPOLOGY: linear
207
--> 208 ~~(ii) TYPE OF MOLECULE: peptide~~
209
210 (iii) HYPOTHETICAL: NO
211
212 (iv) ANTI-SENSE: YES
213
214 (v) FRAGMENT TYPE: internal fragment
215
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

217
218 Val Trp Asp Val Asp Tyr Ser Ala Phe Asp Ala Asn His Cys Ser
219 1 5 10 15
220

Error #4

221 (2) INFORMATION FOR SEQ ID NO: 10:
222
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 15 amino acids
225 (B) TYPE: amino acid
226 (C) STRANDEDNESS: single-stranded
227 (D) TOPOLOGY: linear
228
--> 229 ~~(ii) TYPE OF MOLECULE: peptide~~
230
231 (iii) HYPOTHETICAL: NO
232
233 (iv) ANTI-SENSE: YES
234
235 (v) FRAGMENT TYPE: internal fragment
236
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

238
239 Glu-Asn Lys Arg Ile Thr Val Gly Gly-Met Pro Ser Gly Cys
240 1 5 10 15
241

242 (2) INFORMATION FOR SEQ ID NO: 11:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:08

INPUT SET: S35457.raw

243
244 (i) SEQUENCE CHARACTERISTICS:
245 (A) LENGTH: 15 amino acids
246 (B) TYPE: amino acid
247 (C) STRANDEDNESS: single-stranded
248 (D) TOPOLOGY: linear
249
--> 250 (ii) ~~TYPE OF MOLECULE: peptide~~
251
252 (iii) HYPOTHETICAL: NO
253
254 (iv) ANTI-SENSE: YES
255
256 (v) FRAGMENT TYPE: internal fragment
257
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
259
260 His Phe Lys Ser Leu Gly Gln Thr Ile Thr Pro Ala Asp Lys Ser
261 1 5 10 15
262

263 (2) INFORMATION FOR SEQ ID NO: 12:
264
265 (i) SEQUENCE CHARACTERISTICS:
266 (A) LENGTH: 15 amino acids
267 (B) TYPE: amino acid
268 (C) STRANDEDNESS: single-stranded
269 (D) TOPOLOGY: linear
270
--> 271 (ii) ~~TYPE OF MOLECULE: peptide~~
272
273 (iii) HYPOTHETICAL: NO
274
275 (iv) ANTI-SENSE: YES
276
277 (v) FRAGMENT TYPE: internal fragment
278
279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
280
281 Leu Lys Ala Arg Asp Ile Asn Asp Ile Phe Ala Ile Leu Lys Asn
282 1 5 10 15
283

284 (2) INFORMATION FOR SEQ ID NO: 13:
285
286 (i) SEQUENCE CHARACTERISTICS:
287 (A) LENGTH: 15 amino acids
288 (B) TYPE: amino acid
289 (C) STRANDEDNESS: single-stranded
290 (D) TOPOLOGY: linear
291
--> 292 (ii) ~~TYPE OF MOLECULE: peptide~~
293

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:08

INPUT SET: S35457.raw

294 (iii) HYPOTHETICAL: NO
295
296 (iv) ANTI-SENSE: YES
297
298 (v) FRAGMENT TYPE: internal fragment
299
300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
301
302 Ser Glu Glu Lys Phe Val Thr Met Thr Asp Leu Val Pro Gly Ile
303 1 5 10 15
304

305 (2) INFORMATION FOR SEQ ID NO: 14:
306
307 (i) SEQUENCE CHARACTERISTICS:
308 (A) LENGTH: 15 amino acids
309 (B) TYPE: amino acid
310 (C) STRANDEDNESS: single-stranded
311 (D) TOPOLOGY: linear
312
--> 313 ~~(ii) TYPE OF MOLECULE: peptide~~
314
315 (iii) HYPOTHETICAL: NO
316
317 (iv) ANTI-SENSE: YES
318
319 (v) FRAGMENT TYPE: internal fragment
320
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
322
323 Val Thr Met Thr Asp Leu Val Pro Gly Ile Leu Glu Lys Gln Arg
324 1 5 10 15
325

326 (2) INFORMATION FOR SEQ ID NO: 15:
327
328 (i) SEQUENCE CHARACTERISTICS:
329 (A) LENGTH: 15 amino acids
330 (B) TYPE: amino acid
331 (C) STRANDEDNESS: single-stranded
332 (D) TOPOLOGY: linear
333
--> 334 ~~(ii) TYPE OF MOLECULE: peptide~~
335
336 (iii) HYPOTHETICAL: NO
337
338 (iv) ANTI-SENSE: YES
339
340 (v) FRAGMENT TYPE: internal fragment
341
342 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
343
344 Thr Gly Phe Ile Pro Pro Met Ala Ser Leu Glu Asp Lys Gly Lys

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:08

INPUT SET: S35457.raw

345 1 5 10 15
346

347 (2) INFORMATION FOR SEQ ID NO: 16:

348

349 (i) SEQUENCE CHARACTERISTICS:

350 (A) LENGTH: 15 amino acids

351 (B) TYPE: amino acid

352 (C) STRANDEDNESS: single-stranded

353 (D) TOPOLOGY: linear

354

--> 355 ~~(ii) TYPE OF MOLECULE: peptide~~

356

357 (iii) HYPOTHETICAL: NO

358

359 (iv) ANTI-SENSE: YES

360

361 (v) FRAGMENT TYPE: internal fragment

362

363 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

364

365 Pro Asn Thr Ser Gly Leu Glu Thr Arg Val Val Gln Ala Glu Arg

366 1 5 10 15

367

368 (2) INFORMATION FOR SEQ ID NO: 17:

369

370 (i) SEQUENCE CHARACTERISTICS:

371 (A) LENGTH: 15 amino acids

372 (B) TYPE: amino acid

373 (C) STRANDEDNESS: single-stranded

374 (D) TOPOLOGY: linear

375

--> 376 ~~(ii) TYPE OF MOLECULE: peptide~~

377

378 (iii) HYPOTHETICAL: NO

379

380 (iv) ANTI-SENSE: YES

381

382 (v) FRAGMENT TYPE: internal fragment

383

384 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

385

386 Glu Leu Tyr Gln Leu Thr Leu Phe Pro His Gln Phe Ile Asn Pro

387 1 5 10 15

388

389 (2) INFORMATION FOR SEQ ID NO: 18:

390

391 (i) SEQUENCE CHARACTERISTICS:

392 (A) LENGTH: 15 amino acids

393 (B) TYPE: amino acid

394 (C) STRANDEDNESS: single-stranded

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:09

INPUT SET: S35457.raw

395 (D) TOPOLOGY: linear
396
--> 397 (ii) ~~TYPE OF MOLECULE: peptide~~
398
399 (iii) HYPOTHETICAL: NO
400
401 (iv) ANTI-SENSE: YES
402
403 (v) FRAGMENT TYPE: internal fragment
404
405 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
406
407 Val Met Val Val Ala Pro Leu Thr Val Asn Thr Glu Gly Ala Pro
408 1 5 10 15
409

410 (2) INFORMATION FOR SEQ ID NO: 19:
411
412 (i) SEQUENCE CHARACTERISTICS:
413 (A) LENGTH: 15 amino acids
414 (B) TYPE: amino acid
415 (C) STRANDEDNESS: single-stranded
416 (D) TOPOLOGY: linear
417
--> 418 (ii) ~~TYPE OF MOLECULE: peptide~~
419
420 (iii) HYPOTHETICAL: NO
421
422 (iv) ANTI-SENSE: YES
423
424 (v) FRAGMENT TYPE: internal fragment
425
426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
427
428 Leu Ala Gly Leu Ala Gln Tyr Tyr Thr Gln Tyr Ser Gly Thr Ile
429 1 5 10 15
430
431

432 (2) INFORMATION FOR SEQ ID NO: 20:
433
434 (i) SEQUENCE CHARACTERISTICS:
435 (A) LENGTH: 15 amino acids
436 (B) TYPE: amino acid
437 (C) STRANDEDNESS: single-stranded
438 (D) TOPOLOGY: linear
439
--> 440 (ii) ~~TYPE OF MOLECULE: peptide~~
441
442 (iii) HYPOTHETICAL: NO
443
444 (iv) ANTI-SENSE: YES
445

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:09

INPUT SET: S35457.raw

446 (v) FRAGMENT TYPE: internal fragment

447

448 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

449

450 Glu Thr Thr Asn Val Gln Gly Trp Val Cys Leu Phe Gln Ile Thr

451 1 5 10 15

452

453 (2) INFORMATION FOR SEQ ID NO: 21:

454

455 (i) SEQUENCE CHARACTERISTICS:

456 (A) LENGTH: 15 amino acids

457 (B) TYPE: amino acid

458 (C) STRANDEDNESS: single-stranded

459 (D) TOPOLOGY: linear

460

--> 461 (ii) ~~TYPE OF MOLECULE: peptide~~

462

463 (iii) HYPOTHETICAL: NO

464

465 (iv) ANTI-SENSE: YES

466

467 (v) FRAGMENT TYPE: internal fragment

468

469 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

470

471 Gln Gly Trp Val Cys Leu Phe Gln Ile Thr His Gly Lys Ala Asp

472 1 5 10 15

473

474 (2) INFORMATION FOR SEQ ID NO: 22:

475

476 (i) SEQUENCE CHARACTERISTICS:

477 (A) LENGTH: 15 amino acids

478 (B) TYPE: amino acid

479 (C) STRANDEDNESS: single-stranded

480 (D) TOPOLOGY: linear

481

--> 482 (ii) ~~TYPE OF MOLECULE: peptide~~

483

484 (iii) HYPOTHETICAL: NO

485

486 (iv) ANTI-SENSE: YES

487

488 (v) FRAGMENT TYPE: internal fragment

489

490 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

491

492 Tyr Asn Arg Asn Ala Val Pro Asn Leu Arg Gly Asp Leu Gln Val

493 1 5 10 15

494

495

496 (2) INFORMATION FOR SEQ ID NO: 23:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:10

INPUT SET: S35457.raw

497
498 (i) SEQUENCE CHARACTERISTICS:
499 (A) LENGTH: 15 amino acids
500 (B) TYPE: amino acid
501 (C) STRANDEDNESS: single-stranded
502 (D) TOPOLOGY: linear
503
--> 504 (ii) ~~TYPE OF MOLECULE: peptide~~
505
506 (iii) HYPOTHETICAL: NO
507
508 (iv) ANTI-SENSE: YES
509
510 (v) FRAGMENT TYPE: internal fragment
511
512 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
513
514 Glu Ile Lys Ala Leu Phe Leu Ser Arg Thr Thr Gly Lys Met Glu
515 1 5 10 15
516

517 (2) INFORMATION FOR SEQ ID NO: 24:
518
519 (i) SEQUENCE CHARACTERISTICS:
520 (A) LENGTH: 15 amino acids
521 (B) TYPE: amino acid
522 (C) STRANDEDNESS: single-stranded
523 (D) TOPOLOGY: linear
524
--> 525 (ii) ~~TYPE OF MOLECULE: peptide~~
526
527 (iii) HYPOTHETICAL: NO
528
529 (iv) ANTI-SENSE: YES
530
531 (v) FRAGMENT TYPE: internal fragment
532
533 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
534
535 Cys Trp Leu Asn Ala Ile Leu Gln Leu Phe Arg Tyr Val Glu Glu
536 1 5 10 15
537

538 (2) INFORMATION FOR SEQ ID NO: 25:
539
540 (i) SEQUENCE CHARACTERISTICS:
541 (A) LENGTH: 15 amino acids
542 (B) TYPE: amino acid
543 (C) STRANDEDNESS: single-stranded
544 (D) TOPOLOGY: linear
545
--> 546 (ii) ~~TYPE OF MOLECULE: peptide~~
547

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:10

INPUT SET: S35457.raw

548 (iii) HYPOTHETICAL: NO
549
550 (iv) ANTI-SENSE: YES
551
552 (v) FRAGMENT TYPE: internal fragment
553
554 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
555
556 Arg Tyr Val Glu Glu Pro Phe Phe Asp Trp Val Tyr Ser Ser Pro
557 1 5 10 15
558
559

560 (2) INFORMATION FOR SEQ ID NO: 26:
561
562 (i) SEQUENCE CHARACTERISTICS:
563 (A) LENGTH: 15 amino acids
564 (B) TYPE: amino acid
565 (C) STRANDEDNESS: single-stranded
566 (D) TOPOLOGY: linear
567
--> 568 ~~(ii) TYPE OF MOLECULE: peptide~~
569
570 (iii) HYPOTHETICAL: NO
571
572 (iv) ANTI-SENSE: YES
573
574 (v) FRAGMENT TYPE: internal fragment
575
576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
577
578 Glu Ala Ile Lys Gln Leu Glu Asp Leu Thr Gly Leu Glu Leu His
579 1 5 10 15
580

581 (2) INFORMATION FOR SEQ ID NO: 27:
582
583 (i) SEQUENCE CHARACTERISTICS:
584 (A) LENGTH: 15 amino acids
585 (B) TYPE: amino acid
586 (C) STRANDEDNESS: single-stranded
587 (D) TOPOLOGY: linear
588
--> 589 ~~(ii) TYPE OF MOLECULE: peptide~~
590
591 (iii) HYPOTHETICAL: NO
592
593 (iv) ANTI-SENSE: YES
594
595 (v) FRAGMENT TYPE: internal fragment
596
597 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
598

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:10

INPUT SET: S35457.raw

599 Asn-Ile-Lys-His-Leu-Leu-His-Thr-Gly-Ile-Gly-Thr-Ala-Ser-Arg
600 1 5 10 15
601

602 (2) INFORMATION FOR SEQ ID NO: 28:

603

604 (i) SEQUENCE CHARACTERISTICS:

605 (A) LENGTH: 15 amino acids

606 (B) TYPE: amino acid

607 (C) STRANDEDNESS: single-stranded

608 (D) TOPOLOGY: linear

609

--> 610 (ii) ~~TYPE OF MOLECULE: peptide~~

611

612 (iii) HYPOTHETICAL: NO

613

614 (iv) ANTI-SENSE: YES

615

616 (v) FRAGMENT TYPE: internal fragment

617

618 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

619

620 Ala-Ile-Asp-Asp-Glu-Asp-Phe-Tyr-Pro-Trp-Thr-Pro-Asp-Pro-Ser

621 1 5 10 15

622

623

624 (2) INFORMATION FOR SEQ ID NO: 29:

625

626 (i) SEQUENCE CHARACTERISTICS:

627 (A) LENGTH: 15 amino acids

628 (B) TYPE: amino acid

629 (C) STRANDEDNESS: single-stranded

630 (D) TOPOLOGY: linear

631

--> 632 (ii) ~~TYPE OF MOLECULE: peptide~~

633

634 (iii) HYPOTHETICAL: NO

635

636 (iv) ANTI-SENSE: YES

637

638 (v) FRAGMENT TYPE: internal fragment

639

640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

641

642 Thr-Pro-Asp-Pro-Ser-Asp-Val-Leu-Val-Phe-Val-Pro-Tyr-Asp-Gln

643 1 5 10 15

644

645 (2) INFORMATION FOR SEQ ID NO: 30:

646

647 (i) SEQUENCE CHARACTERISTICS:

--> 648 (A) LENGTH: 15 amino acids

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:11

INPUT SET: S35457.raw

649 (B) TYPE: amino acid
650 (C) STRANDEDNESS: single-stranded
651 (D) TOPOLOGY: linear
652
--> 653 (ii) ~~TYPE OF MOLECULE: peptide~~
654
655 (iii) HYPOTHETICAL: NO
656
657 (iv) ANTI-SENSE: YES
658
659 (v) FRAGMENT TYPE: internal fragment
660
661 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30
662
--> 663 Thr Asp Leu Gln Lys Mt Val Met Gly Asn Thr Lys Pro Val Glu
664 1 5 10 15
665

Error

invalid amino descriptor (met)?

666 (2) INFORMATION FOR SEQ ID NO: 31:
667
668 (i) SEQUENCE CHARACTERISTICS:
669 (A) LENGTH: 15 amino acids
670 (B) TYPE: amino acid
671 (C) STRANDEDNESS: single-stranded
672 (D) TOPOLOGY: linear
673
--> 674 (ii) ~~TYPE OF MOLECULE: peptide~~
675
676 (iii) HYPOTHETICAL: NO
677
678 (iv) ANTI-SENSE: YES
679
680 (v) FRAGMENT TYPE: internal fragment
681
682 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
683
684 Met Leu Ser Asp Ala Ala Leu Met Val Leu His Arg Gly Asn Arg
685 1 5 10 15
686
687

688 (2) INFORMATION FOR SEQ ID NO: 32:
689
690 (i) SEQUENCE CHARACTERISTICS:
691 (A) LENGTH: 15 amino acids
692 (B) TYPE: amino acid
693 (C) STRANDEDNESS: single-stranded
694 (D) TOPOLOGY: linear
695
--> 696 (ii) ~~TYPE OF MOLECULE: peptide~~
697
698 (iii) HYPOTHETICAL: NO
699

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:11

INPUT SET: S35457.raw

700 (iv) ANTI-SENSE: YES
701
702 (v) FRAGMENT TYPE: internal fragment
703
704 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
705
706 Leu Leu Lys Met Lys Ala His Ile Asp Pro Glu Pro His His Glu
707 1 5 10 15
708

709 (2) INFORMATION FOR SEQ ID NO: 33:
710
711 (i) SEQUENCE CHARACTERISTICS:
712 (A) LENGTH: 15 amino acids
713 (B) TYPE: amino acid
714 (C) STRANDEDNESS: single-stranded
715 (D) TOPOLOGY: linear
716
--> 717 ~~(ii) TYPE OF MOLECULE: peptide~~
718
719 (iii) HYPOTHETICAL: NO
720
721 (iv) ANTI-SENSE: YES
722
723 (v) FRAGMENT TYPE: internal fragment
724
725 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
726
727 Pro Phe Phe Phe Ser Asp Val Arg Ser Asn Phe Ser Lys Leu Val
728 1 5 10 15
729

730 (2) INFORMATION FOR SEQ ID NO: 34:
731
732 (i) SEQUENCE CHARACTERISTICS:
733 (A) LENGTH: 14 amino acids
734 (B) TYPE: amino acid
735 (C) STRANDEDNESS: single-stranded
736 (D) TOPOLOGY: linear
737
--> 738 ~~(ii) TYPE OF MOLECULE: peptide~~
739
740 (iii) HYPOTHETICAL: NO
741
742 (iv) ANTI-SENSE: YES
743
744 (v) FRAGMENT TYPE: internal fragment
745
746 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
747
748 Ala Pro Val Leu Leu Ala Gly Leu Val Lys Val Ala Ser Ser
749 1 5 10
750

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:11

INPUT SET: S35457.raw

751

752 (2) INFORMATION FOR SEQ ID NO: 35:

753

754 (i) SEQUENCE CHARACTERISTICS:

755 (A) LENGTH: 14 amino acids

756 (B) TYPE: amino acid

757 (C) STRANDEDNESS: single-stranded

758 (D) TOPOLOGY: linear

759

--> 760 (ii) ~~TYPE OF MOLECULE: peptide~~

761

762 (iii) HYPOTHETICAL: NO

763

764 (iv) ANTI-SENSE: YES

765

766 (v) FRAGMENT TYPE: internal fragment

767

768 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

769

770 Ala Gly Leu Val Lys Val Ala Ser Ser Phe Phe Arg Ser Thr

771 1 5 10

772

773 (2) INFORMATION FOR SEQ ID NO: 36:

774

775 (i) SEQUENCE CHARACTERISTICS:

776 (A) LENGTH: 14 amino acids

777 (B) TYPE: amino acid

778 (C) STRANDEDNESS: single-stranded

779 (D) TOPOLOGY: linear

780

--> 781 (ii) ~~TYPE OF MOLECULE: peptide~~

782

783 (iii) HYPOTHETICAL: NO

784

785 (iv) ANTI-SENSE: YES

786

787 (v) FRAGMENT TYPE: internal fragment

788

789 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

790

791 Val Ala Ser Ser Phe Phe Arg Ser Thr Pro Glu Asp Leu Glu

792 1 5 10

793

794 (2) INFORMATION FOR SEQ ID NO: 37:

795

796 (i) SEQUENCE CHARACTERISTICS:

797 (A) LENGTH: 14 amino acids

798 (B) TYPE: amino acid

799 (C) STRANDEDNESS: single-stranded

800 (D) TOPOLOGY: linear

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:12

INPUT SET: S35457.raw

801
--> 802 ~~(ii) TYPE OF MOLECULE: peptide~~
803
804 (iii) HYPOTHETICAL: NO
805
806 (iv) ANTI-SENSE: YES
807
808 (v) FRAGMENT TYPE: internal fragment
809
810 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
811
812 Phe Phe Arg Ser Thr Pro Glu Asp Leu Glu Arg Ala Glu Lys
813 1 5 10
814
815

816 (2) INFORMATION FOR SEQ ID NO: 38:
817
818 (i) SEQUENCE CHARACTERISTICS:
819 (A) LENGTH: 14 amino acids
820 (B) TYPE: amino acid
821 (C) STRANDEDNESS: single-stranded
822 (D) TOPOLOGY: linear
823
--> 824 ~~(ii) TYPE OF MOLECULE: peptide~~
825
826 (iii) HYPOTHETICAL: NO
827
828 (iv) ANTI-SENSE: YES
829
830 (v) FRAGMENT TYPE: internal fragment
831
832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
833
834 Ile Ser Ile Pro Ser Gln Lys Ser Val Leu Tyr Phe Leu Ile
835 1 5 10
836

837 (2) INFORMATION FOR SEQ ID NO: 39:
838
839 (i) SEQUENCE CHARACTERISTICS:
840 (A) LENGTH: 14 amino acids
841 (B) TYPE: amino acid
842 (C) STRANDEDNESS: single-stranded
843 (D) TOPOLOGY: linear
844
--> 845 ~~(ii) TYPE OF MOLECULE: peptide~~
846
847 (iii) HYPOTHETICAL: NO
848
849 (iv) ANTI-SENSE: YES
850
851 (v) FRAGMENT TYPE: internal fragment

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:12

INPUT SET: S35457.raw

852
853 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
854
855 Lys Arg Gln Lys Met Val Asp Asp Ala Val Asn Glu Tyr Ile
856 1 5 10
857

858 (2) INFORMATION FOR SEQ ID NO: 40:
859
860 (i) SEQUENCE CHARACTERISTICS:
861 (A) LENGTH: 14 amino acids
862 (B) TYPE: amino acid
863 (C) STRANDEDNESS: single-stranded
864 (D) TOPOLOGY: linear
865
--> 866 ~~(ii) TYPE OF MOLECULE: peptide~~
867
868 (iii) HYPOTHETICAL: NO
869
870 (iv) ANTI-SENSE: YES
871
872 (v) FRAGMENT TYPE: internal fragment
873
874 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
875
876 Asn Glu Tyr Ile Glu Lys Ala Asn Ile Thr Thr Asp Asp Lys
877 1 5 10
878
879

880 (2) INFORMATION FOR SEQ ID NO: 41:
881
882 (i) SEQUENCE CHARACTERISTICS:
883 (A) LENGTH: 14 amino acids
884 (B) TYPE: amino acid
885 (C) STRANDEDNESS: single-stranded
886 (D) TOPOLOGY: linear
887
--> 888 ~~(ii) TYPE OF MOLECULE: peptide~~
889
890 (iii) HYPOTHETICAL: NO
891
892 (iv) ANTI-SENSE: YES
893
894 (v) FRAGMENT TYPE: internal fragment
895
896 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
897
898 Thr Asp Asp Lys Thr Leu Asp Glu Ala Glu Lys Ser Pro Leu
899 1 5 10
900

901 (2) INFORMATION FOR SEQ ID NO: 42:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:12

INPUT SET: S35457.raw

902
903 (i) SEQUENCE CHARACTERISTICS:
904 (A) LENGTH: 14 amino acids
905 (B) TYPE: amino acid
906 (C) STRANDEDNESS: single-stranded
907 (D) TOPOLOGY: linear
908
--> 909 (ii) ~~TYPE OF MOLECULE: peptide~~
910
911 (iii) HYPOTHETICAL: NO
912
913 (iv) ANTI-SENSE: YES
914
915 (v) FRAGMENT TYPE: internal fragment
916
917 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
918
919 Thr Val Gly Phe Arg Glu Arg Thr Leu Pro Gly Gln Lys Ala
920 1 5 10
921

922 (2) INFORMATION FOR SEQ ID NO: 43:
923
924 (i) SEQUENCE CHARACTERISTICS:
925 (A) LENGTH: 14 amino acids
926 (B) TYPE: amino acid
927 (C) STRANDEDNESS: single-stranded
928 (D) TOPOLOGY: linear
929
--> 930 (ii) ~~TYPE OF MOLECULE: peptide~~
931
932 (iii) HYPOTHETICAL: NO
933
934 (iv) ANTI-SENSE: YES
935
936 (v) FRAGMENT TYPE: internal fragment
937
938 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
939
940 Asp Asp Val Asn Ser Glu Pro Ala Gln Pro Val Glu Glu Gln
941 1 5 10
942
943

944 (2) INFORMATION FOR SEQ ID NO: 44:
945
946 (i) SEQUENCE CHARACTERISTICS:
947 (A) LENGTH: 14 amino acids
948 (B) TYPE: amino acid
949 (C) STRANDEDNESS: single-stranded
950 (D) TOPOLOGY: linear
951
--> 952 (ii) ~~TYPE OF MOLECULE: peptide~~

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:13

INPUT SET: S35457.raw

953
954 (iii) HYPOTHETICAL: NO
955
956 (iv) ANTI-SENSE: YES
957
958 (v) FRAGMENT TYPE: internal fragment
959
960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
961
962 Asn Thr Gly Ser Ile Ile Asn Asn Tyr Tyr Met Gln Gln Tyr
963 1 5 10
964

965 (2) INFORMATION FOR SEQ ID NO: 45:

966
967 (i) SEQUENCE CHARACTERISTICS:
968 (A) LENGTH: 14 amino acids
969 (B) TYPE: amino acid
970 (C) STRANDEDNESS: single-stranded
971 (D) TOPOLOGY: linear

--> 972
973 (ii) ~~TYPE OF MOLECULE: peptide~~

974
975 (iii) HYPOTHETICAL: NO
976
977 (iv) ANTI-SENSE: YES
978
979 (v) FRAGMENT TYPE: internal fragment
980

981 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

982
983 Gly Pro Tyr Ala Gly Pro Leu Glu Arg Gln Lys Pro Leu Lys
984 1 5 10
985

986 (2) INFORMATION FOR SEQ ID NO: 46:

987
988 (i) SEQUENCE CHARACTERISTICS:
989 (A) LENGTH: 14 amino acids
990 (B) TYPE: amino acid
991 (C) STRANDEDNESS: single-stranded
992 (D) TOPOLOGY: linear

--> 993
994 (ii) ~~TYPE OF MOLECULE: peptide~~

995
996 (iii) HYPOTHETICAL: NO
997
998 (iv) ANTI-SENSE: YES
999
1000 (v) FRAGMENT TYPE: internal fragment
1001

1002 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

1003

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:13

INPUT SET: S35457.raw

1004 Pro Leu Glu Arg Gln Lys Pro Leu Lys Val Arg Ala Lys Leu
1005 1 5 10
1006
1007

1008 (2) INFORMATION FOR SEQ ID NO: 47:

1009

1010 (i) SEQUENCE CHARACTERISTICS:

1011 (A) LENGTH: 14 amino acids

1012 (B) TYPE: amino acid

1013 (C) STRANDEDNESS: single-stranded

1014 (D) TOPOLOGY: linear

1015

--> 1016 (ii) ~~TYPE OF MOLECULE: peptide~~

1017

1018 (iii) HYPOTHETICAL: NO

1019

1020 (iv) ANTI-SENSE: YES

1021

1022 (v) FRAGMENT TYPE: internal fragment

1023

1024 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

1025

1026 Gly Pro Tyr Ala Gly Pro Met Glu Arg Gln Lys Pro Leu Lys

1027 1

1028

1029 (2) INFORMATION FOR SEQ ID NO: 48:

1030

1031 (i) SEQUENCE CHARACTERISTICS:

1032 (A) LENGTH: 14 amino acids

1033 (B) TYPE: amino acid

1034 (C) STRANDEDNESS: single-stranded

1035 (D) TOPOLOGY: linear

1036

--> 1037 (ii) ~~TYPE OF MOLECULE: peptide~~

1038

1039 (iii) HYPOTHETICAL: NO

1040

1041 (iv) ANTI-SENSE: YES

1042

1043 (v) FRAGMENT TYPE: internal fragment

1044

1045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

1046

1047 Pro Met Glu Arg Gln Lys Pro Leu Lys Val Lys Ala Lys Ala

1048 1 5 10 10

1049

1050

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:13

INPUT SET: S35457.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i)APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Bayer Aktiengesellschaft
27	Unknown or Misplaced Identifier	(A) CURRENT APPLICATION NUMBER:09/254,966
28	Unknown or Misplaced Identifier	(B) CURRENT APPLICATION FILING DATE: March 16
29	Unknown or Misplaced Identifier	(C) PRIOR APPLICATION NUMBER:PCT/EP97/04866
30	Unknown or Misplaced Identifier	(D) PRIOR APPLICATION FILING DATE:September 8, 1
40	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
61	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
82	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
103	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
124	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
145	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
166	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
187	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
208	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
229	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
250	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
271	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
292	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
313	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
334	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
355	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
376	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
397	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
418	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
440	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
461	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
482	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
504	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
525	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
546	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
568	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
589	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
610	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
632	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
648	Entered (15) and Calc. Seq. Length (14) differ	(A) LENGTH: 15 amino acids
653	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
663	Wrong Amino Acid Designator	Thr Asp Leu Gln Lys Mt Val Met Gly Asn Thr Lys Pro Val
674	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
696	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
717	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
738	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
760	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
781	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
802	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
824	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
845	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
866	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:14**INPUT SET: S35457.raw**

Line	Error	Original Text
888	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
909	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
930	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
952	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
973	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
994	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
1016	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
1037	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/254,966DATE: 01/25/2001
TIME: 23:33:14

INPUT SET: S35457.raw

Line	Original Text	Corrected Text
17	(E) ZIP CODE:15205-9741	(E) ZIP:15205-9741
20	(v)COMPUTER-READABLE FORM:	(v) COMPUTER READABLE FORM:
44	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
65	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
86	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
107	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
128	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
149	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
170	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
191	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
212	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
233	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
254	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
275	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
296	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
317	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
338	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
359	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
380	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
401	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
422	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
444	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
465	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
486	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
508	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
529	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
550	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
572	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
593	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
614	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
636	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
657	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
678	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
700	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
721	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
742	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
764	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
785	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
806	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
828	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
849	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
870	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
892	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
913	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
934	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
956	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
977	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
998	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES

PAGE: 2

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/254,966

DATE: 01/25/2001
TIME: 23:33:14

INPUT SET: S35457.raw

Line	Original Text	Corrected Text
1020	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
1041	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES